

### **AMENDMENTS TO THE CLAIMS**

This listing of claims will replace all prior versions and listings of claims in the application.

#### **Listing of Claims:**

1-10. (cancelled)

11. (currently amended) An isolated polynucleotide comprising:

- (a) a nucleotide sequence encoding a polypeptide which is a cytochrome P450 enzyme capable of producing ~~associated with the synthesis of delta12-~~  
~~epoxyepoxygenated~~ fatty acids wherein said polypeptide has at least 50% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2; or
- (b) the complement of the nucleotide sequence, wherein the complement and the nucleotide sequence contain the same number of nucleotides and are 100% complementary.

12. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 55% identity based on the Clustal alignment method.

13. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 60% identity based on the Clustal alignment method.

14. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 65% identity based on the Clustal alignment method.

15. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 70% identity based on the Clustal alignment method.

16. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 75% identity based on the Clustal alignment method.

17. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 80% identity based on the Clustal alignment method.

18. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 85% identity based on the Clustal alignment method.

19. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 90% identity based on the Clustal alignment method.

20. (previously presented) The polynucleotide of Claim 11, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:2 have at least 95% identity based on the Clustal alignment method.

21. (previously presented) The polynucleotide of Claim 11, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:2.

22. (previously presented) The polynucleotide of Claim 11, wherein the nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:1.

23. (previously presented) A host cell comprising the polynucleotide of Claim 11.

24. (previously presented) The host cell of Claim 23, wherein the cell is selected from the group consisting of a yeast cell, a bacterial cell and a plant cell.

25. (cancelled)

~~25~~26. (currently amended) A method for transforming a cell comprising introducing into a cell the polynucleotide of Claim 11.

27. (cancelled)

~~26~~28. (currently amended) A recombinant DNA construct comprising the polynucleotide of Claim 11 operably linked to at least one regulatory sequence.

~~27~~29. (currently amended) A vector comprising the polynucleotide of Claim 11.

30. (cancelled)